



## SEQUENCE LISTING

<110> Fujimoto, Katsumi  
Shin, Mei  
Kato, Yukio

<120> NOVEL bHLH TYPE TRANSCRIPTION FACTOR  
GENES DEC2

<130> 06501-101001

<140> US 10/078,650  
<141> 2002-02-19

<150> PCT/JP00/03991  
<151> 2000-06-19

<150> JP 11-233286  
<151> 1999-08-19

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aacagcagtt gaac atg gac gaa gga att cct cat ttg caa gag aga cag 170  
Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln  
1 5 10

tta ctg gaa cat aga gat ttt ata gga ctg gac tat tcc tct ttg tat 218  
Leu Leu Glu His Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr  
15 20 25

atg tgt aaa ccc aaa agg agc atg aaa cga gac gac acc aag gat acc 266  
Met Cys Lys Pro Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Asp Thr  
30 35 40

tac aaa tta ccg cac aga tta ata gaa aag aaa aga aga gac cga att 314  
Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile  
45 50 55 60

aat gaa tgc att gct cag ctg aaa gat tta ctg cct gaa cat ctg aaa 362  
Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys  
65 70 75

ttg aca act ctg gga cat ctg gag aaa gct gta gtc ttg gaa tta act		410	
Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr			
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ttg aaa cac tta aaa gct tta acc gcc tta acc gag caa cag cat cag		458	
Leu Lys His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln			
95	100	105	
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Lys Ile Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile			
110	115	120	
cag tcc gac ttg gat gcg ttc cac tcg gga ttt caa aca tgc gcc aaa		554	
Gln Ser Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys			
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gaa gtc ttg caa tac ctc tcc cgg ttt gag agc tgg aca ccc agg gag		602	
Glu Val Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu			
145	150	155	
ccg cgg tgt gtc cag ctg atc aac cac ttg cac gcc gtg gcc acc cag		650	
Pro Arg Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln			
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Phe Leu Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys			
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Gly Thr Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Pro Cys Leu			
190	195	200	
gag cgc gcg ggg cag aag ctg gag ccc ctc gcc tac tgc gtg ccc gtc		794	
Glu Arg Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val			
205	210	215	220
atc cag cgg act cag ccc agc gcc gag ctc gcc gcc gag aac gac acg		842	
Ile Gln Arg Thr Gln Pro Ser Ala Glu Leu Ala Glu Asn Asp Thr			
225	230	235	
gac acc gac agc ggc tac ggc ggc gaa gcc gag gcc cgg ccg gac cgc		890	
Asp Thr Asp Ser Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg			
240	245	250	
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Glu Lys Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu			
255	260	265	
cct ccc ggg gag gac tcg ccg gcg ccc aag agg atg aag ctg gat tcc		986	
Pro Pro Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser			
270	275	280	
cgc ggc ggc agc ggc ggc ccg ggg ggc ggc gcg gcg gcg gcg		1034	
Arg Gly Gly Gly Ser Gly Gly Pro Gly Gly Gly Ala Ala Ala Ala			
285	290	295	300

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aga ccc gac gcc gcc ctg ctc agc tcg ctg gtg gcg ttc ggc gga ggc Arg Pro Asp Ala Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly 320	325	330	1130	
gga ggc gcg ccc ttc ccg cag ccc gcg gcc gcc gcg ccc ttc tgc Gly Gly Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Pro Phe Cys 335	340	345	1178	
ctg ccc ttc tgc ttc ctc tcg cct tct gca gct gcc gcc tac gtg cag Leu Pro Phe Cys Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln 350	355	360	1226	
ccc ttc ctg gac aag agc ggc ctg gag aag tat ctg tac ccg gcg gcg Pro Phe Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala 365	370	375	380	1274
gct gcc gcc ccg ttc ccg ctg cta tac ccc ggc atc ccc gcc ccg gcg Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala 385	390	395	1322	
gca gcc gcg gca gcc gcc gcc gct gcc gcc gcc gcc gcc gcg ttc Ala Ala Phe 400	405	410	1370	
ccc tgc ctg tcc tcg gtg ttg tcg ccc cct ccc gag aag gcg ggc gcc Pro Cys Leu Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala 415	420	425	1418	
gcc gcc gcg acc ctc ctg ccg cac gag gtg gcg ccc ctt ggg gcg ccg Ala Ala Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro 430	435	440	1466	
cac ccc cag cac ccg cac ggc cgc acc cac ctg ccc ttc gcc ggg ccc His Pro Gln His Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro 445	450	455	460	1514
cgc gag ccg ggg aac ccg gag agc tct gct cag gaa gat ccc tcg cag Arg Glu Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln 465	470	475	1562	
cca gga aag gaa gct ccc tgaatccttg cgtcccgaaag gacggagggtt Pro Gly Lys Glu Ala Pro 480			1610	
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			2030	
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gactcatct	taatttcttc	taagtccata	tatagataga	tatctatctg	tacagatttc	2450
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ccaatctctt	gcaaggctcc	aggctctggc	tttgcttacc	tgctcgttcc	caatgtatct	3590
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 <212> PRT  
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 Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro  
 35 40 45  
 His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile  
 50 55 60  
 Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu  
 65 70 75 80  
 Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu  
 85 90 95  
 Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala  
 100 105 110  
 Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser Asp Leu  
 115 120 125  
 Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln  
 130 135 140  
 Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Val  
 145 150 155 160  
 Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu Pro Thr  
 165 170 175  
 Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr Gly Ala  
 180 185 190  
 Pro Ser Ala Ala Gly Ser Ala Ala Pro Cys Leu Glu Arg Ala Gly

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Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln Arg Thr		
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Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr Asp Ser		
225	230	235
Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys Gly Lys		
245	250	255
Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro Gly Glu		
260	265	270
Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly Gly Gly		
275	280	285
Ser Gly Gly Pro Gly Gly Ala Ala Ala Ala Ala Ala Ala Leu		
290	295	300
Leu Gly Pro Asp Pro Ala Ala Ala Ala Leu Leu Arg Pro Asp Ala		
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Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly Ala Pro		
325	330	335
Phe Pro Gln Pro Ala Ala Ala Ala Pro Phe Cys Leu Pro Phe Cys		
340	345	350
Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln Pro Phe Leu Asp		
355	360	365
Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala Ala Pro		
370	375	380
Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala Ala Ala		
385	390	395
Ala Phe Pro Cys Leu Ser		
405	410	415
Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala Ala Thr		
420	425	430
Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro Gln His		
435	440	445
Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu Pro Gly		
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&lt;223&gt; Artificially Synthesized Primer Sequence

&lt;400&gt; 9

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26

&lt;210&gt; 10

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Artificially Synthesized Primer Sequence

&lt;400&gt; 10

gcgggggttt tcagtatcta cga

23

&lt;210&gt; 11

&lt;211&gt; 1511

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)...(1453)

&lt;400&gt; 11

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Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His  
1 5 10 15

49

aga gat ttt ata gga ctg gac tat tcc tct ttg tat atg tgt aaa ccc  
Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro  
20 25 30

97

aaa agg agc atg aaa cga gac gac acc aag gta agt gat acc tac aaa  
Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Val Ser Asp Thr Tyr Lys  
35 40 45

145

tta ccg cac aga tta ata gaa aag aaa aga aga gac cga att aat gaa  
Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu  
50 55 60

193

tgc att gct cag ctg aaa gat tta ctg cct gaa cat ctg aaa ttg aca  
Cys Ile Ala Gln Leu Lys Asp Leu Pro Glu His Leu Lys Leu Thr  
65 70 75 80

241

act ctg gga cat ctg gag aaa gct gta gtc ttg gaa tta act ttg aaa  
Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys  
85 90 95

289

cac tta aaa gct tta acc gcc tta acc gag caa cag cat cag aag ata  
His Leu Lys Ala Leu Thr Ala Leu Glu Gln Gln His Gln Lys Ile  
100 105 110

337

att gct tta cag aat ggg gag cga tct ctg aaa tcg ccc att cag tcc Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser 115 120 125	385
gac ttg gat gcg ttc cac tcg gga ttt caa aca tgc gcc aaa gaa gtc Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val 130 135 140	433
ttg caa tac ctc tcc cgg ttt gag agc tgg aca ccc agg gag ccg cgg Leu Gln Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg 145 150 155 160	481
tgt gtc cag ctg atc aac cac ttg cac gcc gtc acc cag ttc ttg Cys Val Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu 165 170 175	529
ccc acc ccg cag ctg ttg act caa cag gtc cct ctg agc aaa ggc acc Pro Thr Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr 180 185 190	577
ggc gct ccc tcg gcc ggg tcc gcg gcc gcc ccc tgc ctg gag cgc Gly Ala Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg 195 200 205	625
gcg ggg cag aag ctg gag ccc ctc gcc tac tgc gtc ccc gtc atc cag Ala Gly Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln 210 215 220	673
cgg act cag ccc agc gcc gag ctc gcc gag aac gac acg gac acc Arg Thr Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr 225 230 235 240	721
gac agc ggc tac ggc ggc gaa gcc gag gcc cgg ccc gac cgc gag aaa Asp Ser Gly Tyr Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys 245 250 255	769
ggc aaa ggc gcg ggg gcg agc cgc gtc acc atc aag cag gag cct ccc Gly Lys Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro 260 265 270	817
ggg gag gac tcg ccg gcg ccc aag agg atg aag ctg gat tcc cgc ggc Gly Glu Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly 275 280 285	865
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gcg ctt ctg ggg ccc gac cct gcc gcc gcg ctg ctg aga ccc Ala Leu Leu Gly Pro Asp Pro Ala Ala Ala Ala Leu Leu Arg Pro 305 310 315 320	961
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gcg ccc ttc ccg cag ccc gcg gcc gcc gcg ccc ttc tgc ctg ccc Ala Pro Phe Pro Gln Pro Ala Ala Ala Ala Ala Pro Phe Cys Leu Pro 340 345 350	1057
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ctg gac aag agc ggc ctg gag aag tat ctg tac ccg gcg gct gcc Leu Asp Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala Ala 370 375 380	1153
gcc ccg ttc ccg ctg cta tac ccc ggc atc ccc gcc ccg gcg gca gcc Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala Ala 385 390 395 400	1201
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gcg acc ctc ctg ccg cac gag gtg gcg ccc ctt ggg gcg ccg cac ccc Ala Thr Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro 435 440 445	1345
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ccg ggg aac ccg gag agc tct gct cag gaa gat ccc tcg cag cca gga Pro Gly Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly 465 470 475 480	1441
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65	70	75	80
Thr Leu Gly His Leu Glu Lys Ala Val Val		Leu Glu Leu Thr Leu Lys	
85		90	95
His Leu Lys Ala Leu Thr Ala Leu	Thr Glu Gln Gln His Gln Lys Ile		
100	105	110	
Ile Ala Leu Gln Asn Gly Glu Arg Ser	Leu Lys Ser Pro Ile Gln Ser		
115	120	125	
Asp Leu Asp Ala Phe His Ser Gly Phe	Gln Thr Cys Ala Lys Glu Val		
130	135	140	
Leu Gln Tyr Leu Ser Arg Phe Glu Ser	Trp Thr Pro Arg Glu Pro Arg		
145	150	155	160
Cys Val Gln Leu Ile Asn His Leu His	Ala Val Ala Thr Gln Phe Leu		
165	170	175	
Pro Thr Pro Gln Leu Leu Thr Gln Gln	Val Pro Leu Ser Lys Gly Thr		
180	185	190	
Gly Ala Pro Ser Ala Ala Gly Ser	Ala Ala Ala Pro Cys Leu Glu Arg		
195	200	205	
Ala Gly Gln Lys Leu Glu Pro Leu Ala	Tyr Cys Val Pro Val Ile Gln		
210	215	220	
Arg Thr Gln Pro Ser Ala Glu Leu Ala	Ala Glu Asn Asp Thr Asp Thr		
225	230	235	240
Asp Ser Gly Tyr Gly Gly Glu Ala	Glu Ala Arg Pro Asp Arg Glu Lys		
245	250	255	
Gly Lys Gly Ala Gly Ala Ser Arg	Val Thr Ile Lys Gln Glu Pro Pro		
260	265	270	
Gly Glu Asp Ser Pro Ala Pro Lys Arg	Met Lys Leu Asp Ser Arg Gly		
275	280	285	
Gly Gly Ser Gly Gly Pro Gly Gly	Ala Ala Ala Ala Ala Ala		
290	295	300	
Ala Leu Leu Gly Pro Asp Pro Ala	Ala Ala Ala Ala Leu Leu Arg Pro		
305	310	315	320
Asp Ala Ala Leu Leu Ser Ser Leu	Val Ala Phe Gly Gly Gly Gly		
325	330	335	
Ala Pro Phe Pro Gln Pro Ala Ala	Ala Ala Pro Phe Cys Leu Pro		
340	345	350	
Phe Cys Phe Leu Ser Pro Ser Ala	Ala Ala Ala Tyr Val Gln Pro Phe		
355	360	365	
Leu Asp Lys Ser Gly Leu Glu Lys	Tyr Leu Tyr Pro Ala Ala Ala Ala		
370	375	380	
Ala Pro Phe Pro Leu Leu Tyr Pro	Gly Ile Pro Ala Pro Ala Ala		
385	390	395	400
Ala Ala Ala Ala Ala Ala Ala	Ala Ala Phe Pro Cys		
405	410	415	
Leu Ser Ser Val Leu Ser Pro Pro	Glu Lys Ala Gly Ala Ala Ala		
420	425	430	
Ala Thr Leu Leu Pro His Glu Val	Ala Pro Leu Gly Ala Pro His Pro		
435	440	445	
Gln His Pro His Gly Arg Thr His	Leu Pro Phe Ala Gly Pro Arg Glu		
450	455	460	
Pro Gly Asn Pro Glu Ser Ser Ala	Gln Glu Asp Pro Ser Gln Pro Gly		
465	470	475	480
Lys Glu Ala Pro			

<210> 13  
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&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (74)...(1303)

&lt;400&gt; 13

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Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln	
1 5 10	
tta ctg gaa cat agg gat ttt ata gga ctg gac tat tcc tct ttg tat	157
Leu Leu Glu His Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr	
15 20 25	
atg tgt aaa ccc aaa agg agc ttg aag cga gac gat acc aag gat acc	205
Met Cys Lys Pro Lys Arg Ser Leu Lys Arg Asp Asp Thr Lys Asp Thr	
30 35 40	
tac aag tta ccg cac aga tta ata gaa aag aag aga cga gac cga att	253
Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile	
45 50 55 60	
aat gaa tgc att gct cag ctg aaa gat tta ctg ccc gaa cat ctg aaa	301
Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys	
65 70 75	
ttg aca aca ctg ggg cat ttg gag aaa gca gta gtc ttg gaa tta act	349
Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr	
80 85 90	
tta aag cac ttg aaa gcg cta aca gcc tta act gag cag cag cat cag	397
Leu Lys His Leu Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln	
95 100 105	
aag ata att gct tta cag aat ggg gag cgc tct ctg aaa tcg ccg gtc	445
Lys Ile Ile Ala Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Val	
110 115 120	
cag gcc gac ttg gat gcg ttc cac tcg ggg ttt caa acc tgc gcc aaa	493
Gln Ala Asp Leu Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys	
125 130 135 140	
gaa gtc ttg caa tac ctc gcg cgc ttt gag agc tgg aca ccc agg gag	541
Glu Val Leu Gln Tyr Leu Ala Arg Phe Glu Ser Trp Thr Pro Arg Glu	
145 150 155	
ccg cgc tgc gca cag ctc gtc agc cac ctg cat gcc gtg gcc acc cag	589
Pro Arg Cys Ala Gln Leu Val Ser His Leu His Ala Val Ala Thr Gln	
160 165 170	
ctc ctg acg cca cag gtg ccc tcc ggc agg ggc tct ggg cgc gcg ccc	637
Leu Leu Thr Pro Gln Val Pro Ser Gly Arg Gly Ser Gly Arg Ala Pro	
175 180 185	
tgc agc gcg ggg gct gcg gcc gcc tcg ggt ccc gag cgc gtc gcc cgc	685

Cys Ser Ala Gly Ala Ala Ala Ser Gly Pro Glu Arg Val Ala Arg			
190	195	200	
tgc gtg ccg gtc atc cag cgg act cag ccc ggc acg gag ccg gaa cac		733	
Cys Val Pro Val Ile Gln Arg Thr Gln Pro Gly Thr Glu Pro Glu His			
205	210	220	
gac acg gac acc gac agc ggc tac gga ggc gag gcg gag cag ggc cgc		781	
Asp Thr Asp Thr Asp Ser Gly Tyr Gly Gly Glu Ala Glu Gln Gly Arg			
225	230	235	
gcg gcc gtc aag cag gag cca ccc ggg gac tcg tcg cct gcg ccc aag		829	
Ala Ala Val Lys Gln Glu Pro Pro Gly Asp Ser Ser Pro Ala Pro Lys			
240	245	250	
agg ccg aag ctg gag gcg cgc ggc gcg ctc ctg ggc ccg gag ccc gcg		877	
Arg Pro Lys Leu Glu Ala Arg Gly Ala Leu Leu Gly Pro Glu Pro Ala			
255	260	265	
ctg ctc ggc tcg ctc gtg gcg ctt ggc ggg ggc gcg ccc ttc gcg cag		925	
Leu Leu Gly Ser Leu Val Ala Leu Gly Gly Ala Pro Phe Ala Gln			
270	275	280	
ccc gct gcc gcg ccc ttc tgc ctg ccc ttc tat ctg ctg tcg ccg tcc		973	
Pro Ala Ala Ala Pro Phe Cys Leu Pro Phe Tyr Leu Leu Ser Pro Ser			
285	290	295	300
gcc gcc gcc tac gta cag ccc tgg cta gac aag agc ggc ctg gac aag		1021	
Ala Ala Ala Tyr Val Gln Pro Trp Leu Asp Lys Ser Gly Leu Asp Lys			
305	310	315	
tat ctg tac ccc gcg gcc gcg ccc ttc ccg ctg ctg tat ccc ggc		1069	
Tyr Leu Tyr Pro Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly			
320	325	330	
atc cca gca gcg gcc gcc gct gct gct gcc gcc gct ttc cct tgc ttg		1117	
Ile Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu			
335	340	345	
tcg tcc gtg ctg tcg cca ccc ccg gag aag gcc ggc gcg acc gcc ggt		1165	
Ser Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Thr Ala Gly			
350	355	360	
gcc ccg ttc ctg gcg cac gag gtg gcg ccc ccg ggg ccg ctg cgc ccc		1213	
Ala Pro Phe Leu Ala His Glu Val Ala Pro Pro Gly Pro Leu Arg Pro			
365	370	375	380
cag cac gcg cat agc cgc acc cac ctg ccg cgc gct gtg aac ccg gag		1261	
Gln His Ala His Ser Arg Thr His Leu Pro Arg Ala Val Asn Pro Glu			
385	390	395	
agc tct cag gaa gat gcc acg cag ccg gcc aag gac gcc ccc		1303	
Ser Ser Gln Glu Asp Ala Thr Gln Pro Ala Lys Asp Ala Pro			
400	405	410	
tgaaccgcg attccttcca gaacaggca gggggctccc gaggagtcgc cgggtttcca		1363	
agttcaaacg tcctctaaag cgtgccagg aggaagagta agcgatgctc gacaggct		1421	

<210> 14  
 <211> 410  
 <212> PRT  
 <213> Mus musculus

<400> 14  
 Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His  
 1 5 10 15  
 Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro  
 20 25 30  
 Lys Arg Ser Leu Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro  
 35 40 45  
 His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile  
 50 55 60  
 Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu  
 65 70 75 80  
 Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu  
 85 90 95  
 Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala  
 100 105 110  
 Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Val Gln Ala Asp Leu  
 115 120 125  
 Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln  
 130 135 140  
 Tyr Leu Ala Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Ala  
 145 150 155 160  
 Gln Leu Val Ser His Leu His Ala Val Ala Thr Gln Leu Leu Thr Pro  
 165 170 175  
 Gln Val Pro Ser Gly Arg Gly Ser Gly Arg Ala Pro Cys Ser Ala Gly  
 180 185 190  
 Ala Ala Ala Ser Gly Pro Glu Arg Val Ala Arg Cys Val Pro Val  
 195 200 205  
 Ile Gln Arg Thr Gln Pro Gly Thr Glu Pro Glu His Asp Thr Asp Thr  
 210 215 220  
 Asp Ser Gly Tyr Gly Gly Glu Ala Glu Gln Gly Arg Ala Ala Val Lys  
 225 230 235 240  
 Gln Glu Pro Pro Gly Asp Ser Ser Pro Ala Pro Lys Arg Pro Lys Leu  
 245 250 255  
 Glu Ala Arg Gly Ala Leu Leu Gly Pro Glu Pro Ala Leu Leu Gly Ser  
 260 265 270  
 Leu Val Ala Leu Gly Gly Ala Pro Phe Ala Gln Pro Ala Ala Ala  
 275 280 285  
 Pro Phe Cys Leu Pro Phe Tyr Leu Leu Ser Pro Ser Ala Ala Ala Tyr  
 290 295 300  
 Val Gln Pro Trp Leu Asp Lys Ser Gly Leu Asp Lys Tyr Leu Tyr Pro  
 305 310 315 320  
 Ala Ala Ala Ala Pro Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Ala  
 325 330 335  
 Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu Ser Ser Val Leu  
 340 345 350  
 Ser Pro Pro Pro Glu Lys Ala Gly Ala Thr Ala Gly Ala Pro Phe Leu  
 355 360 365  
 Ala His Glu Val Ala Pro Pro Gly Pro Leu Arg Pro Gln His Ala His  
 370 375 380  
 Ser Arg Thr His Leu Pro Arg Ala Val Asn Pro Glu Ser Ser Gln Glu  
 385 390 395 400

Asp Ala Thr Gln Pro Ala Lys Asp Ala Pro  
 405 410

<210> 15  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificially Synthesized Primer Sequence

<400> 15  
 aaaatctctc caggcgaccc t

21

<210> 16  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificially Synthesized Primer Sequence

<400> 16  
 agcctgtcga gcatcgctta

20

<210> 17  
 <211> 412  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys  
 1 5 10 15  
 Ala Pro Gly Leu Glu His Gly Asp Leu Pro Gly Met Tyr Pro Ala His  
 20 25 30  
 Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp  
 35 40 45  
 Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg  
 50 55 60  
 Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro  
 65 70 75 80  
 Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val  
 85 90 95  
 Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp  
 100 105 110  
 Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly  
 115 120 125  
 Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser  
 130 135 140  
 Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His  
 145 150 155 160  
 Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His  
 165 170 175  
 Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser  
 180 185 190

Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro  
 195 200 205  
 Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln  
 210 215 220  
 Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp  
 225 230 235 240  
 Thr Asp Ser Gly Tyr Gly Glu Ser Glu Lys Gly Asp Leu Arg Ser  
 245 250 255  
 Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly  
 260 265 270  
 Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys  
 275 280 285  
 Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser  
 290 295 300  
 Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro  
 305 310 315 320  
 Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu  
 325 330 335  
 Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr  
 340 345 350  
 Pro Gly Leu Asn Ala Ser Ala Ala Leu Ser Ser Phe Met Asn Pro  
 355 360 365  
 Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro  
 370 375 380  
 Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu  
 385 390 395 400  
 Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp  
 405 410

<210> 18  
 <211> 253  
 <212> PRT  
 <213> Rattus norvegicus

<400> 18  
 Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His  
 1 5 10 15  
 Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro  
 20 25 30  
 Lys Arg Ser Leu Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro  
 35 40 45  
 His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile  
 50 55 60  
 Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu  
 65 70 75 80  
 Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu  
 85 90 95  
 Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala  
 100 105 110  
 Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Val Gln Ala Asp Leu  
 115 120 125  
 Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln  
 130 135 140  
 Tyr Leu Ala Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Ala  
 145 150 155 160  
 Gln Leu Val Ser His Leu His Ala Val Ala Thr Gln Leu Leu Thr Pro  
 165 170 175

Gln Val Thr Pro Gly Arg Gly Pro Gly Arg Ala Pro Cys Ser Ala Gly  
180 185 190  
Ala Ala Ala Ala Ser Gly Ser Glu Arg Val Ala Arg Cys Val Pro Val  
195 200 205  
Ile Gln Arg Thr Gln Pro Gly Thr Glu Pro Glu His Asp Thr Asp Thr  
210 215 220  
Asp Ser Gly Tyr Gly Gly Glu Ala Glu Gln Gly Arg Ala Ala Val Lys  
225 230 235 240  
Gln Glu Pro Pro Gly Asp Pro Ser Leu Arg Pro Arg Gly  
245 250